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Attorney Docket No. 15966-581 CIP
(Cura-81 CIP)



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANTS: Kerry E. Quinn et al.
SERIAL NUMBER: 09/996,015 EXAMINER: Not yet assigned
FILING DATE: November 28, 2001 ART UNIT: Not yet assigned
FOR: AORTIC CARBOXYPEPTIDASE-LIKE PROTEINS AND NUCLEIC ACIDS
ENCODING SAME

Commissioner for Patents
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Prior to examination of the above-identified application, please amend the application as set forth below and consider the following remarks:

In the Specification:

Replace the first full paragraph on page 6:

“FIG. 4 is a comparison showing regions of identity and of conserved amino acid substitutions in the amino acid sequences of a mouse CPPX1 polypeptide (AFO77738) and the ACPL1a polypeptide (SEQ ID NO:2) (ALO35460_GENESCAN_predicted_pep”).”

with the following re-written paragraph:

-- FIG. 4 is a comparison showing regions of identity and of conserved amino acid substitutions in the amino acid sequences of a mouse CPPX1 polypeptide (AFO77738) (SEQ ID NO:13) and the ACPL1a polypeptide (SEQ ID NO:2) (ALO35460_GENESCAN_predicted_pep”).--

A marked-up version showing changes made to the specification is submitted herewith as **Appendix A**, pursuant to 37 C.F.R. § 1.121(b)(1)(iii).

Please insert the sequence listing, pages 1-51, at the end of the specification.

In the Drawings:

Pursuant to 37 C.F.R. § 1.121(d), Applicants submit herewith, in **Appendix B**, separate sheets of drawings showing proposed changes in red. Specifically, Applicants wish to cancel Figure 2 of the present application and insert new Figure 2. Applicants further wish to amend Figures 14, 15, and 16. Applicants respectfully request Examiner's approval of these changes.

Applicants additionally submit herewith, in **Appendix C**, drawings in compliance with 37 C.F.R. § 1.84, incorporating the above changes.

REMARKS

In response to the Notice to File Missing Parts of Nonprovisional Application, Applicants submit herein an initial computer readable form (CRF) copy of the "Sequence Listing," and an initial paper copy of the "Sequence Listing." No new matter has been added. A statement that the content of the paper and computer readable copies are the same and include no new matter, in compliance with 37 C.F.R. §§ 1.821 – 1.825 is also included.

The Specification has been amended to insert the sequence listing and to add a sequence identifier number. Figure 2 of the present application has been canceled because it contains errors. Support for new Figure 2 appears in U.S.S.N. 09/641,741, filed August 18, 2000, (the '741 application). The present application claims priority to the '741 application and incorporates the '741 application by reference (*See, e.g.*, page 1 of the present application). Thus, no new matter has been added.

Additionally, Figures 14-16 misidentify sequences. The drawings have been amended to

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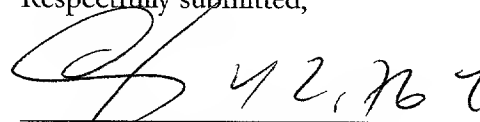
correct these informalities and to comply with the requirements of 37 C.F.R. § 1.84. No new matter has been added.

A petition for a two-month extension of time is submitted herewith. Applicants believe that no additional fee is due with the submission of this Response. However, the Commissioner is hereby authorized to charge any fees that may be due, or credit any overpayment of same, to Deposit Account No. 50-0311, Reference No. 15966-581 CIP (Cura-81 CIP).

CONCLUSION

On the basis of the foregoing amendments and remarks, Applicants respectfully submit that the pending claims are in condition for allowance. If there are any questions regarding this submission, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,



Ivor R. Elrifi, Reg. No. 39,529

Attorney for Applicant

c/o MINTZ, LEVIN, COHN, FERRIS,

GLOVSKY & POPEO, P.C.

One Financial Center

Boston, Massachusetts 02111

Tel: (617) 542-6000

Fax: (617) 542-2241

Dated: May 8, 2002

APPENDIX A

In the Specification:

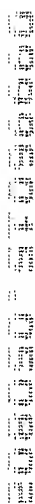
On page 6, first full paragraph:

FIG. 4 is a comparison showing regions of identity and of conserved amino acid substitutions in the amino acid sequences of a mouse CPPX1 polypeptide (AFO77738) (SEQ ID NO:13) and the ACPL1a polypeptide (SEQ ID) (ALO35460_GENESCAN_predicted_pep”).

TRA 1651068v1

APPENDIX B

PROPOSED AMENDMENTS TO FIGURES



Cancel

MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETAN
GTSEQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGC
PPLGLESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDA
DPWFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSS
GMDAVFPANSDPETPVLNLLPEPQVARFIRLLPQTLWLQGGAPCLRAEILACPVS
PNDLFLEAPASGSSDPLDFQHNYKAMRKLKQVQEQCPNITRIYSIGKSYQGLKLYVME
MSDKPGEHELGEPEORYEAGMHGNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIH
LLPSMNPDGYEIAYHRGSELVGWAEGRWNNQSIDLNNFADLNTPLWEAODDGKVP
HIVPNHHLPLPTYYTLPNATVAPETRAVIKWMKRI PFVLSANLHGGELVVSYPFDMTR
TPWAARELTPTPDDAVFRWLSTVYAGSNLAMQDTSRRPCHSODFSVHGNIINGADW
HTVPGSMNDFSYLHTNCFEVTVELSCDKFPHENELPQEWENNKDALLTYLEQVRMGI
AGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDYWRLLTPGDYMTASAEQYHS
VTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLRRRLERLRGQKD

Fig. 2

Insert

-- Figure 2. Protein sequence encoded by the coding sequence shown in Figure 1.

MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETA
NGTSEQHVRIKVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQET
GCPPLGLESRLVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEE
QDADPWFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGS
RNHSSGMDAVFPANSDPETPVLNLLPEPQVARFIRLLPQTWLQGGAPCLRAEIL
ACPVSDPNDFLEAPASGSSDPLDFQHNYKAMRKLMKQVQECPNITRIYSIGKSYQ
GLKLYMEMSDKPGEHELGEPEVRYVAGMHGNEALGRELLLLMQFLCHEFLRGNPRV
TRLLSEMRIHLLPSMNPDGYEIA YHRGSELVGWAEGRWNNQSIDLNHNFADLNTPLW
EAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETRAVIKWMKRIPFVLSANLHGGE
LVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSNLAMQDTSRRPCHSQDF
SVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHENELPQEWENNKD
ALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDYWRLTPG
DYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLR
RRLERLRGQKD --

Figure 14.

>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 2735 (962.8 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 510/510 (100%), Positives = 510/510 (100%)

Query: 1 MWGLLLAALAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
MWGLLLAALAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct: 1 MWGLLLAALAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL
Sbjct: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120

Query: 121 ESLRVSDSRLEASSQSFGGLGPHRGRLNIQSGLEDGDLVDGAWCAEEQDADPWFQVDAGH 180
ESLRVSDSRLEASSQSFGGLGPHRGRLNIQSGLEDGDLVDGAWCAEEQDADPWFQVDAGH
Sbjct: 121 ESLRVSDSRLEASSQSFGGLGPHRGRLNIQSGLEDGDLVDGAWCAEEQDADPWFQVDAGH 180

Query: 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
Sbjct: 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Query: 241 NLLPEPQVARFIRLLPQTLQGGAPCLRAEILACPVSNDPNDLFLEAPASGSSDPLDFQHH 300
NLLPEPQVARFIRLLPQTLQGGAPCLRAEILACPVSNDPNDLFLEAPASGSSDPLDFQHH
Sbjct: 241 NLLPEPQVARFIRLLPQTLQGGAPCLRAEILACPVSNDPNDLFLEAPASGSSDPLDFQHH 300

Query: 301 NYKAMRKLKMQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHELGEPEVRYVAGMH 360
NYKAMRKLKMQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHELGEPEVRYVAGMH
Sbjct: 301 NYKAMRKLKMQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHELGEPEVRYVAGMH 360

Query: 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG
Sbjct: 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420

Query: 421 WAEGRWNNQSIDLNNHFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480
WAEGRWNNQSIDLNNHFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR
Sbjct: 421 WAEGRWNNQSIDLNNHFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480

Query: 481 AVIKWMKRIPFVLSANLHGGELVVSYPFDM 510 (SEQ ID NO: 45)
AVIKWMKRIPFVLSANLHGGELVVSYPFDM
Sbjct: 481 AVIKWMKRIPFVLSANLHGGELVVSYPFDM 510

Score = 341 (120.0 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 67/69 (97%), Positives = 67/69 (97%)

Query: 507 PFD-MVTASAEGYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPPDLRRR 565
P D MVTASAEGYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPPDLRRR
Sbjct: 666 PGDYMVTASAEGYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPPDLRRR 725

Query: 566 LERLRGQKD 574 (SEQ ID NO: 6) (SEQ ID NO: 46)
LERLRGQKD (SEQ ID NO: 41)
Sbjct: 726 LERLRGQKD 734 (SEQ ID NO: 42)

Figure 15

>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 1005 (353.8 bits), Expect = 4.4e-101, P = 4.4e-101
Identities = 192/193 (99%), Positives = 193/193 (100%)

Query: 1 MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct: 1 MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
Sbjct: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

Query: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query: 181 PTRFSGVITQGRD 193 [(SEQ ID NO:8)] (SEQ ID NO:47)
PTRFSGVITQGR+ (SEQ ID NO:43)
Sbjct: 181 PTRFSGVITQGRN 193 (SEQ ID NO:44)

Figure 16

>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 3952 (1391.2 bits), Expect = 0.0, P = 0.0
Identities = 734/734 (100%), Positives = 734/734 (100%)

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Query:      1 MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
            MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct:      1 MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query:     61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120
            EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL
Sbjct:     61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120

Query:    121 ESLRVSDSRLEASSSQSFLGPHRGRLNIQSGLEDGDLYDGAWCAEQDADPWFQVDAGH 180
            ESLRVSDSRLEASSSQSFLGPHRGRLNIQSGLEDGDLYDGAWCAEQDADPWFQVDAGH
Sbjct:    121 ESLRVSDSRLEASSSQSFLGPHRGRLNIQSGLEDGDLYDGAWCAEQDADPWFQVDAGH 180

Query:    181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
            PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
Sbjct:    181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Query:    241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
            NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
Sbjct:    241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query:    301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYMEMSDKPGHEHELGEPEVRYVAGMH 360
            NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYMEMSDKPGHEHELGEPEVRYVAGMH
Sbjct:    301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYMEMSDKPGHEHELGEPEVRYVAGMH 360

Query:    361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420
            GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG
Sbjct:    361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420

Query:    421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETR 480
            WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETR
Sbjct:    421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETR 480

Query:    481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540
            AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
Sbjct:    481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540

Query:    541 LAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600
            LAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
Sbjct:    541 LAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600

Query:    601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660
            NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
Sbjct:    601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660

Query:    661 WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720
            WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
Sbjct:    661 WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720

Query:    721 DLRRRLERLRGQKD 734 (SEQ ID NO:2)
            DLRRRLERLRGQKD [(SEQ ID NO:45)]
Sbjct:    721 DLRRRLERLRGQKD 734 [(SEQ ID NO:46)]

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APPENDIX C

SUBSTITUTE DRAWINGS